PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Patent Application
of Ian Hector Frazer *et al.*   :

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For: METHOD AND POLYNUCLEOTIDES   : Attorney Docket
              FOR DETERMINING TRANSLATIONAL   : No. **10338-5 US**
              EFFICIENCY OF A CODON   : (2423066/VPA)

**CLAIM OF FOREIGN PRIORITY AND
TRANSMITTAL OF PRIORITY DOCUMENT**

Applicants hereby confirm their claim of the right of foreign priority under 35 U.S.C. Section 119 for the above-identified patent application. The claim of foreign priority is based upon Application No. PP 8078, filed in Australia on January 8, 1999, and International Application No. PCT/AU00/00008, filed in Australian on January 7, 2000, and the benefit of those dates is claimed.

Submitted herewith are certified copies of both Australian Applications identified in the paragraph above. It is submitted that these documents complete the requirements of 35 U.S.C. Section 119, and benefit of the foreign priority is respectfully requested.

Respectfully submitted,

IAN HECTOR FRAZER *ET AL.*

_Oct. 24, 2001____ By: _____
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I, GAYE TURNER, TEAM LEADER EXAMINATION SUPPORT AND SALES hereby certify that annexed is a true copy of the Provisional specification in connection with Application No. PP 8078 for a patent by THE UNIVERSITY OF QUEENSLAND filed on 08 January 1999.

WITNESS my hand this
Fifth day of October 2001

GAYE TURNER
<u>TEAM LEADER EXAMINATION</u>
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AUSTRALIA

Patents Act 1990

PROVISIONAL SPECIFICATION

Invention Title: "CODON UTILIZATION"

The invention is described in the following statement:

TITLE

"CODON UTILIZATION"

FIELD OF THE INVENTION

THIS INVENTION relates generally to gene expression and in particular, a method and polynucleotides for determining codon utilization in one or more cells or tissues of an organism. More particularly, the method and polynucleotides of the invention are concerned with ascertaining codon preferences in cells or tissues for purposes of modifying the translational efficiency of protein-encoding polynucleotides in those cells or tissues.

BACKGROUND OF THE INVENTION

It is well known that a "triplet" codon of four possible nucleotide bases can exist in 64 variant forms. These forms provide the message for only 20 different amino acids (as well as translation initiation and termination) and this means that some amino acids can be encoded by more than one codon. In this context, some amino acids have as many as six "redundant", alternative codons while some others have a single, required codon.

For reasons not completely understood, codon utilization is highly biased in that alternative codons are not at all uniformly present in the endogenous DNA of differing cell types. In this regard, there appears to exist a variable natural hierarchy of "preference" for certain codons between different cell types or between different organisms.

Codon usage patterns have been shown to correlate with relative abundance of isoaccepting transfer RNA (iso-tRNA) species, and with genes encoding proteins of high versus low abundance. Moreover, the present inventors recently discovered that the intracellular abundance of different iso-tRNAs varies in different cells or tissues of a single multi-cellular organism (see copending International Application No. PCT/AU98/00530).

The implications of codon preference phenomena on gene expression are manifest in that these phenomena can affect the translational efficiency of messenger RNA (mRNA). In this regard, it is widely known that translation of "rare codons", for which the corresponding iso-tRNA is in relatively low abundance, may cause a ribosome to pause during translation which can lead to a failure to complete a nascent polypeptide chain and an uncoupling of transcription and translation.

A primary goal in recombinant research is to provide transgenic organisms which express a foreign gene in an amount sufficient to confer the desired phenotype to the organism. However, expression of the foreign gene may be severely impeded if a particular host cell of the organism or the organism itself has a low abundance of iso-tRNAs corresponding to one or more codons of the foreign gene. Accordingly, a major aim of investigators in this field is to first ascertain the codon preference for particular cells or tissues in which a foreign gene is to be expressed, and subsequently alter the codon composition of the foreign gene for optimized expression in those cells or tissues.

Codon preference may be determined simply by analyzing the frequency at which codons are used by genes expressed by a particular cell or tissue or by a

plurality of cells or tissues of a given organism. Codon frequency tables as well as suitable methods for determining frequency of codon usage in an organism are described, for example, in an article by Sharp *et al* (1988, *Nucleic Acids Res.* **16** 8207-8211). The relative level of gene expression (*e.g.*, detectable protein expression versus no detectable protein expression) can provide an indirect measure of the relative abundance of specific iso-tRNAs expressed in different cells or tissues.

Alternatively, codon preference may be determined by measuring the relative intracellular abundance of different iso-tRNA species. For example, reference may be made to copending International Application No. PCT/AU98/00530 which describes a method that utilizes labeled oligonucleotides specific for different iso-tRNAs to probe an RNA extract prepared from a particular cell or tissue type.

The above methods provide useful indirect evidence for determining codon preference. However, such indirect evidence may not provide an accurate indication of the translational efficiency of a given codon. Accordingly, there is a need to provide a method which more directly ascertains the translational efficiency of a codon in a cell or tissue.

OBJECT OF THE INVENTION

It is therefore an object of the present invention to provide a method for determining codon preference in cells or tissues which method ameliorates at least some of the disadvantages associated with the prior art.

SUMMARY OF THE INVENTION

Accordingly, in one aspect of the invention, there is provided a method for determining relative preference for a codon in at least one cell or tissue type, said method including the steps of:-

(A) introducing into said at least one cell or tissue type a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of identical codons corresponding to said codon under test, wherein said reporter polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to one or more regulatory nucleotide sequences;

(B) expressing said synthetic construct in said at least one cell or tissue type; and

(C) measuring activity associated with said reporter protein in said at least one cell or tissue type to thereby determine the relative preference for said codon.

Preferably, the method is further characterized by the steps of:-

(i) introducing into another of said at least one cell or tissue type a different synthetic construct having said reporter polynucleotide fused in frame with a tandem repeat of identical codons corresponding to a different codon under test, wherein said different codon is synonymous with said first-mentioned codon, and wherein said different synthetic construct is operably linked to one or more regulatory nucleotide sequences;

(ii) expressing said different synthetic construct in said another of said at least one cell or tissue type;

(iii)   measuring activity associated with said reporter protein in said another of said at least one cell or tissue type; and

(iv)   comparing the respective activities associated with said reporter protein from said synthetic constructs to thereby determine the preference for said first-mentioned codon relative to the preference for said different codon.

Preferably, step (A) of the above method is further characterized by the steps of:-

(a)   introducing the synthetic construct into a progenitor cell or tissue of said at least one cell or tissue type; and

(b)   generating said at least one cell or tissue type from said progenitor cell or tissue;

wherein said at least one cell or tissue type contains said synthetic construct.

Suitably, the method is further characterized by the steps of:-

(1)   introducing the synthetic construct into a progenitor cell or tissue of said at least one cell or tissue type; and

(2)   growing an organism or part thereof from said progenitor cell or tissue;

wherein said organism comprises said at least one cell or tissue type containing said synthetic construct.

The method may be further characterized by the step of introducing the synthetic construct into an organism or part thereof such that said synthetic construct is introduced into said at least one cell or tissue type.

In another aspect, the invention resides in a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of identical codons, wherein said reporter polynucleotide

encodes a reporter protein, and wherein said synthetic construct is operably linked to one or more regulatory nucleotide sequences

DETAILED DESCRIPTION

By "expressing said synthetic construct" is meant transcribing the synthetic construct such that mRNA is produced.

The term "synonymous codon" as used herein refers to a codon having a different nucleotide sequence to an existing codon but encoding the same amino acid as the existing codon.

By "isoaccepting transfer RNA" or "iso-tRNA" is meant one or more transfer RNA molecules that differ in their anticodon structure but are specific for the same amino acid.

The term "polynucleotide" as used herein designates mRNA, RNA, cRNA, cDNA or DNA.

The term "progenitor cell or tissue" as used herein refers to a cell or tissue that can gives rise to a particular cell or tissue in which codon preference is to be determined.

Throughout this specification, unless the context requires otherwise, the words "comprise", comprises" and "comprising" will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers.

The present invention is based on the discovery that different stretches of identical codons fused respectively in frame with a reporter polynucleotide can give rise to different levels of reporter protein expressed within a given cell type. Not wishing to be bound by theory, it is believed that a tandem series of identical codons may cause a

ribosome to pause during translation if the iso-tRNA corresponding to the identical codons is limiting. In this regard, it is well known that ribosomal pausing leads to a failure to complete a nascent polypeptide chain and an uncoupling of transcription and translation. Accordingly, the levels of reporter protein expressed in the different cells or tissues will be sensitive to the intracellular abundance of the iso-tRNA species corresponding to the identical codons and will therefore provide a direct correlation a cell's or tissue's preference for a given codon. This means for example, that if the levels of the reporter protein obtained in a cell or tissue type are lower with a synthetic construct having a tandem series of identical first codons compared to those expressed in the same cell or tissue type with a different synthetic construct having a tandem series of identical second codons, wherein the first codons are different to, but synonymous with, the second codons, then it can be deduced that the cell or tissue has a higher preference for the second codon relative to the first codon with respect to translation.

Suitably, the tandem repeat comprises at least three identical codons. Preferably, the tandem repeat comprises four identical codons, more preferably five, six, or seven identical codons. However, it will be appreciated that the number of identical codons utilized for the synthetic construct may vary depending, for example, on the regulatory sequences used to express the synthetic construct, the reporter polynucleotide employed, and the cell or tissue under test. Accordingly, it is preferred that preliminary experiments be carried out to determine an optimal number of identical codons which is sensitive to the intracellular abundance of the corresponding iso-tRNA species, when expressed as part of the

synthetic construct. In this regard, too many identical codons may completely inhibit expression of the reporter protein whilst too few may not influence reporter protein expression at all.

5   The tandem repeat may be fused at a location adjacent to, or within, the reporter polynucleotide. The location is preferably selected such that the tandem repeat interferes with translation of at least a portion of the reporter protein from which an 10   activity can be measured. Preferably, the tandem repeat is located immediately upstream of the reporter polynucleotide.

The reporter polynucleotide may encode any suitable protein whose levels may be determined 15   directly, or indirectly such as by suitable assay. Suitable reporter polynucleotides include, but are not restricted to, polynucleotides encoding β-galactosidase, firefly luciferase, alkaline phosphatase, chloramphenicol acetyltransferase (CAT), 20 β-glucuronidase (GUS), herbicide resistance genes such as the bialophos resistance (BAR) gene that confers resistance to the herbicide BASTA, and green fluorescent protein (GFP). Assays for the activities associated with such proteins are well known by those 25   of skill in the art. Preferably, the reporter polynucleotide encodes GFP.

Of course it will be appreciated that reporter polynucleotides need not correspond to a full-length gene encoding a particular reporter 30   protein. Accordingly, the invention also contemplates reporter polynucleotide sub-sequences encoding desired portions of the reporter protein. A polynucleotide sub-sequence encodes a domain of the reporter protein having an activity associated 35   therewith and preferably encodes at least 10, 20, 50,

100, 150, or 500 contiguous amino acids of the reporter protein.

The method of the invention is applicable to any suitable cell or tissue type. For example, the cell or tissue type may be of mammalian or plant origin. The cell or tissue type may be of any suitable lineage. Suitable cell lines may include, for example, CV-1 cells, COS cells, yeast or spodoptera cells which are capable of being grown *in vitro*. The invention also contemplates cells which may be prokaryotic in origin.

Suitable methods for isolating particular cells or tissues are well known to those of skill in the art. For example, one can take advantage of one or more particular characteristics of a cell or tissue to specifically isolate the cell or tissue from a heterogeneous population. Such characteristics include, but are not limited to, anatomical location of a tissue, cell density, cell size, cell morphology, cellular metabolic activity, cell uptake of ions such as Ca^{2+}, K^+, and H^+ ions, cell uptake of compounds such as stains, markers expressed on the cell surface, protein fluorescence, and membrane potential. Suitable methods that may be used in this regard include surgical removal of tissue, flow cytometry techniques such as fluorescence-activated cell sorting (FACS), immunoaffinity separation (*e.g.*, magnetic bead separation such as Dynabead™ separation), density separation (*e.g.*, metrizamide, Percoll™, or Ficoll™ gradient centrifugation), and cell-type specific density separation.

In an alternate embodiment, progenitor cells or tissues may be used for initially introducing the synthetic construct. Any suitable progenitor cell or tissue may be used which gives rise to a particular

cell or tissue of interest for which codon preference is to be ascertained. For example, a suitable progenitor cell may comprise an undifferentiated cell. In the case of a plant, a suitable progenitor cell may

5 include, for example, a meristematic cell whereas a progenitor tissue may include, for example, a callus tissue.

In another embodiment, the synthetic construct may be introduced firstly into an organism

10 or part thereof before subsequent expression of the construct in a particular cell or tissue type. Any suitable organism is contemplated by the invention which may include unicellular as well as multi-cellular organisms. Exemplary multi-cellular

15 organisms include mammals and plants.

The construction of the synthetic construct may be effected by any suitable technique. For example, *in vitro* mutagenesis methods may be employed which are well known to those of skill in the art.

20 Suitable mutagenesis methods are described for example in the relevant sections of CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (Ausubel, *et al.*, eds.) (John Wiley & Sons, Inc. 1997), and of MOLECULAR CLONING. A LABORATORY MANUAL (Sambrook, *et al.*, eds.) (Cold

25 Spring Harbor Press, 1989), which are incorporated herein by reference. Alternatively, suitable methods for altering DNA are set forth, for example, in U.S. Patent Nos. 4,184,917, 4,321,365 and 4,351,901, which are incorporated herein by reference. Instead of *in*

30 *vitro* mutagenesis, the synthetic polynucleotide may be synthesized *de novo* using readily available machinery. Sequential synthesis of DNA is described, for example, in U.S. Patent No 4,293,652, which is incorporated herein by reference. However, it should be noted that

35 the present invention is not dependent on and not

directed to any one particular technique for constructing the synthetic construct.

Regulatory nucleotide sequences which may be utilized to regulate expression of the synthetic polynucleotide include, but are not limited to, a promoter, an enhancer, and a transcriptional terminator. Such regulatory sequences are well known to those of skill in the art. Suitable promoters which may be utilized to induce expression of the polynucleotides of the invention include constitutive promoters and inducible promoters.

Synthetic constructs according to the invention may be operably linked to one or more regulatory sequences in the form of an expression vector. By "vector" is meant a nucleic acid molecule, preferably a DNA molecule derived, for example, from a plasmid, bacteriophage, or plant virus, into which a synthetic nucleic acid sequence may be inserted or cloned. A vector preferably contains one or more unique restriction sites and may be capable of autonomous replication in a defined host cell including a target cell or tissue or a progenitor cell or tissue thereof, or be integratable with the genome of the defined host such that the cloned sequence is reproducible. Thus, by "expression vector" is meant any autonomous element capable of directing the synthesis of a protein. Such expression vectors are well known by practitioners in the art.

The vector may also include a selection marker such as an antibiotic resistance gene which can be used for selection of suitable transformants/transfectants. Examples of such resistance genes include the *nptII* gene which confers resistance to the antibiotics kanamycin and G418

(Geneticin®) and the *hph* gene which confers resistance to the antibiotic hygromycin B.

The step of introducing the synthetic construct into a particular cell or tissue type, or into a progenitor cell or tissue thereof, or into an organism or part thereof for subsequent introduction into a particular cell or tissue, will differ depending on the intended use and or species, and may involve lipofection, electroporation, micro-projectile bombardment infection by *Agrobacterium tumefaciens* or *A rhizogenes*, or protoplast fusion. Such methods are well known to those skilled in the art.

Alternatively, the step of introduction may involve non-viral and viral vectors, cationic liposomes, retroviruses and adenoviruses such as, for example, described in Mulligan, R.C., (1993 *Science* **260** 926-932) which is incorporated herein by reference. Such methods may include:

(i) Local application of the synthetic nucleic acid sequence by injection (Wolff *et al.*, 1990, *Science* **247** 1465-1468, which is incorporated herein by reference), surgical implantation, instillation or any other means. This method may also be used in combination with local application by injection, surgical implantation, instillation or any other means, of cells responsive to the reporter protein encoded by the synthetic construct. This method may also be used in combination with local application by _ injection, surgical implantation, instillation or any other means, of another factor or factors required for the activity of said reporter protein.

(ii) General systemic delivery by injection of DNA, (Calabretta *et al.*, 1993, *Cancer Treat. Rev.* **19** 169-179, which is incorporated herein

by reference), or RNA, alone or in combination with liposomes (Zhu *et al.*, 1993, *Science* **261** 209-212, which is incorporated herein by reference), viral capsids or nanoparticles (Bertling *et al.*, 1991, *Biotech. Appl. Biochem.* **13** 390-405, which is incorporated herein by reference) or any other mediator of delivery. Improved targeting might be achieved by linking the synthetic construct to a targeting molecule (the so-called "magic bullet" approach employing for example, an antibody), or by local application by injection, surgical implantation or any other means, of another factor or factors required for the activity of the protein produced from said synthetic construct, or of cells responsive to said reporter protein.

(iii) Injection or implantation or delivery by any means, of cells that have been modified *ex vivo* by transfection (for example, in the presence of calcium phosphate: Chen *et al.*, 1987, *Mole. Cell Biochem.* **7** 2745-2752, or of cationic lipids and polyamines: Rose *et al.*, 1991, *BioTech.* **10** 520-525, which articles are incorporated herein by reference), infection, injection, electroporation (Shigekawa *et al.*, 1988, *BioTech.* **6** 742-751, which is incorporated herein by reference) or any other way so as to increase the expression of said synthetic construct in those cells. The modification may be mediated by plasmid, bacteriophage, cosmid, viral (such as adenoviral or retroviral; Mulligan, 1993, *Science* **260** 926-932; Miller, 1992, *Nature* **357** 455-460; Salmons *et al.*, 1993, *Hum. Gen. Ther.* **4** 129-141, which articles are incorporated herein by reference) or other vectors, or other agents of modification such as liposomes (Zhu *et al.*, 1993, *Science* **261** 209-212, which is incorporated herein by reference), viral

capsids or nanoparticles (Bertling *et al.*, 1991, *Biotech. Appl. Biochem.* **13** 390-405, which is incorporated herein by reference), or any other mediator of modification. The use of cells as a delivery vehicle for genes or gene products has been described by Barr *et al.*, 1991, *Science* **254** 1507-1512 and by Dhawan *et al.*, 1991, *Science* **254** 1509-1512, which articles are incorporated herein by reference. Treated cells may be delivered in combination with any nutrient, growth factor, matrix or other agent that will promote their survival in the treated subject.

Advantageously, the relative preference for different codons may be determined by comparing the respective activities of the reporter protein in a given cell or tissue type. One of ordinary skill in the art will thereby be able to determine a relative codon preference table for the cell or tissue type.

The invention further contemplates cells or tissues containing therein the synthetic construct of the invention, or alternatively, cells or tissues produced from the method of the invention.

The invention is further described with reference to the following non-limiting examples.

EXAMPLE 1

Construction of expression vectors for determining relative codon preferences in mammalian cells.

Synthetic *gfp* genes will be constructed in which a single artificial start codon (ATG) followed by a stretch of five identical codons is fused in frame immediately upstream of a *gfp* coding sequence. A reverse oligonucleotide primer (SEQ ID NO:180; sequence complementary to the termination codon for GFP, is underlined), and a suite of forward

oligonucleotide primers (SEQ ID NO: 121 through 179; the first codon of GFP, is underlined) will be synthesized and used for PCR amplification of a humanized *gfp* gene (SEQ ID NO:119) (GIBCO) as template

5　　　with *Taq* DNA polymerase (Amplification parameters: 95°C/30 sec; 52°C/30 sec; 72°C/1 min; 30 cycles). The amplified fragments will have nucleic acid sequences and deduced amino acid sequences as shown in SEQ ID NO:1 through 120. In summary, the synthetic fragments

10　　　contain an artificial start codon followed by a tandem repeat of five identical codons specific for a given iso-tRNA species. The tandem repeat immediately precedes the second codon of the *gfp* gene. The synthetic fragments by SEQ ID NO and encoded tandem

15　　　repeat are presented in the TABLE 1.

TABLE 1. Synthetic fragments and tandem repeats encoded thereby.

SEQ ID NO	Tandem repeat	SEQ ID NO	Tandem repeat
1	Ala (GCA) x 5	61	Leu (CTC) x 5
3	Ala (GCC) x 5	63	Leu (CTG) x 5
5	Ala (GCG) x 5	65	Leu (CTT) x 5
7,	Ala (GCT) x 5	67	Leu (TTA) x 5
9	Arg (AGA) x 5	69	Leu (TTG) x 5
11	Arg (AGG) x 5	71	Lys (AAA) x 5
13	Arg (CGA) x 5	73	Lys (AAG) x 5
15	Arg (CGC) x 5	75	Phe (CTT) x 5
17	Arg (CGG) x 5	77	Phe (TTC) x 5
19	Arg (CGT) x 5	79	Pro (CCC) x 5
21	Asn (AAC) x 5	81	Pro (CCG) x 5
23	Asn (AAT) x 5	83	Pro (CCT) x 5
25	Asp (GAC) x 5	85	Pro (CGA) x 5
27	Asp (GAT) x 5	87	Ser (AGC) x 5
29	Cys (TGC) x 5	89	Ser (AGT) x 5

31	Cys (TGT) x 5	91	Ser (TCA) x 5
33	Gln (CAA) x 5	93	Ser (TCC) x 5
35	Gln (CAG) x 5	95	Ser (TCG) x 5
37	Gly (GAA) x 5	97	Ser (TCT) x 5
39	Glu (GAG) x 5	99	Thr (ACA) x 5
41	Gly (GGA) x 5	101	Thr (ACC) x 5
43	Gly (GGC) x 5	103	Thr (ACG) x 5
45	Gly (GGG) x 5	105	Thr (ACT) x 5
47	Gly (GGT) x 5	107	Trp (TGG) x 5
49	His (CAC) x 5	109	Tyr (TAT) x 5
51	His (CAT) x 5	111	Val (GTA) x 5
53	Ile (ATA) x 5	113	Val (GTC) x 5
55	Ile (ATC) x 5	115	Val (GTG) x 5
57	Ile (ATT) x 5	117	Val (GTT) x 5
59	Leu (CTA) x 5	119	control

The amplified fragments will be cloned between the *Eco*RI and *Kpn*I sites of the mammalian expression vector pCDNA3 containing SV40 *ori* (Invitrogen) and the CMV promoter.

EXAMPLE 2
Transfection of Cos-1 cells

Cos-1 cells in 6-well plates will be transfected with 2 µg of the above expression constructs using lipofectamine (Gibco). GFP fluorescence will be analyzed 36 hrs after transfection. Synthetic *gfp* mRNA expression of transfected cells will also be tested by reverse transcriptase PCR.

EXAMPLE 3
Confocal microscopy

Transfected CV-1 cells can be examined using a Bio-Rad MRC-600 laser-scanning confocal microscope

equipped with a krypton-argon laser and filter sets suitable for the detection of fluorescein and Texas red dyes (Bio-Rad K1yK2), and a Nikon 603 PlanApo numerical aperture 1.2 water-immersion objective. Dual-channel confocal images and video montages of the transfected cells can be suitably composed using ADOBE PhotoShop.

The present invention has been described in terms of particular embodiments found or proposed by the present inventors to comprise preferred modes for the practice of the invention. Those of skill in the art will appreciate that, in light of the present disclosure, numerous modifications and changes may be made in the particular embodiments exemplified without departing from the scope of the invention.

SEQUENCE LISTING

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<170> PatentIn Ver. 2.0

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```
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Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt     96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                    85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
               100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
           115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
       130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
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                    165                    170                    175

      gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
5             180                 185                 190

      atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
      Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
10            195                 200                 205

      cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
      Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
              210                 215                 220

15    ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                 230                 235                 240

      ctg tac aag tga                                                    732
20    Leu Tyr Lys
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30     1               5                  10                  15

      Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                  20                  25                  30

35    Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                  35                  40                  45

      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
              50                  55                  60

40    Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65                  70                  75                  80

      Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
45                    85                  90                  95

      Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                  100                 105                 110

50    Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                  115                 120                 125

      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
              130                 135                 140

55    Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                 150                 155                 160

      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
60                    165                 170                 175

      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                  180                 185                 190

65    Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                  195                 200                 205

      Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
              210                 215                 220

70    Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
```

225   230   235   240

Leu Tyr Lys

5

```
<210> 3
<211> 732
<212> DNA
<213> Artificial Sequence
```

10

```
<220>
<223> Description of Artificial Sequence: Ala(GCC)5GFP
```

```
<220>
```
15
```
<221> CDS
<222> (1)..(732)
```

```
<400> 3
atg gcc gcc gcc gcc agc aag ggc gag gaa ctg ttc act ggc gtg    48
```
20
```
Met Ala Ala Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                   10                  15
```

```
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
```
25
```
            20                  25                  30
```

```
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45
```
30
```
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60
```

35
```
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80
```

```
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
```
40
```
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95
```

```
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
```
45
```
            100                 105                 110
```

```
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125
```
50
```
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140
```

55
```
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160
```

```
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
```
60
```
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175
```

```
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
```
65
```
            180                 185                 190
```

```
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195                 200                 205
```
70
```
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
```

```
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210             215             220

 5      ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag      720
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225             230             235             240

        ctg tac aag tga                                                      732
        Leu Tyr Lys
10


        <210> 4
        <211> 243
        <212> PRT
15      <213> Artificial Sequence

        <400> 4
        Met Ala Ala Ala Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5              10              15
20
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                    20              25              30

        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
25              35              40              45

        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
            50              55              60

30      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
            65              70              75              80

        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                    85              90              95
35
        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                    100             105             110

        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
40              115             120             125

        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130             135             140

45      Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145             150             155             160

        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165             170             175
50
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180             185             190

        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
55                  195             200             205

        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210             215             220

60      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225             230             235             240

        Leu Tyr Lys

65
        <210> 5
        <211> 732
        <212> DNA
        <213> Artificial Sequence
70
        <220>
```

<223> Description of Artificial Sequence: Ala(GCG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 5

```
atg gcg gcg gcg gcg gcg agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Ala Ala Ala Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 6
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 6
Met Ala Ala Ala Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys


<210> 7
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ala(GCT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 7
atg gct gct gct gct gct agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Ala Ala Ala Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
    1               5                   10                  15
```

```
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30
```

5
```
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45
```

10
```
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
            50                  55                  60
```

```
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
     65                  70                  75                  80
```

15

```
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95
```

20
```
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110
```

25
```
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125
```

30
```
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                 135                 140
```

```
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160
```

35

```
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175
```

40
```
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190
```

45
```
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205
```

```
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210                 215                 220
```

50

```
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240
```

55

```
ctg tac aag tga                                                   732
Leu Tyr Lys
```

60

```
<210> 8
<211> 243
<212> PRT
<213> Artificial Sequence
```

65

```
<400> 8
Met Ala Ala Ala Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                   10                  15
```

70
```
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30
```

```
                  Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                          35              40                  45

5                 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                          50              55                  60

                  Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
                  65              70                  75                  80
10
                  Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                                  85                  90                  95

15                Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                              100             105             110

                  Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                          115      .       120                 125

20                Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                              130             135             140

                  Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
                  145             150                 155                 160
25
                  Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                                  165             170             175

                  Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
30                            180             185             190

                  Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                              195             200             205

35                Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                              210             215             220

                  Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
                  225             230                 235                 240
40
                  Leu Tyr Lys
```

```
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65              70              75              80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
             85              90              95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
             100             105             110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
         115             120             125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
     130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
             165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
             180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
             195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
     210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                     732
Leu Tyr Lys


<210> 10
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 10
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1              5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
```

```
                    85                    90                    95
    Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100   .                105.       .         110
    Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115             120             125
    Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130             135             140
    Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
    145             150             155             160
    Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                    165             170             175
    Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180             185             190
    Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195             200             205
    Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210             215             220
    Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
    225             230             235             240
    Leu Tyr Lys
```

<210> 11
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(AGG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 11

```
atg agg agg agg agg agg agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
```

```
                    100                    105                    110

  5   acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
      Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
              115                120                125

      gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 10           130                135                140

      aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
      Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                150                155                160
 15
      aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                170                175

      gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
 20   Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                  180                185                190

      atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
      Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
 25           195                200                205

      cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
      Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
              210                215                220
 30
      ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                230                235                240

 35   ctg tac aag tga                                                     732
      Leu Tyr Lys


      <210> 12
 40   <211> 243
      <212> PRT
      <213> Artificial Sequence

      <400> 12
 45   Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
        1               5                10                15

      Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                      20                25                30
 50
      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                  35                40                45

      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 55           50                55                60

      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65                70                75                80

 60   Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                      85                90                95

      Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                  100                105                110
 65
      Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
              115                120                125

      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 70           130                135                140
```

```
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150             155             160
```

5
```
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175
```

```
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190
```

10
```
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205
```

```
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220
```

15
```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240
```

20
```
Leu Tyr Lys
```

```
<210> 13
<211> 732
<212> DNA
```
25
```
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Arg(CGA)5GFP
```

30
```
<220>
<221> CDS
<222> (1)..(732)
```

```
<400> 13
```
35
```
atg cga cga cga cga cga agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15
```

```
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
40               20                  25                  30
```

```
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
45           35                  40                  45
```

```
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60
```

50
```
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80
```

55
```
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95
```

```
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
60              100             105             110
```

```
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
65          115             120             125
```

```
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130             135             140
```

70
```
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
```

```
      Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                 150                 155                 160

  5   aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                 170                 175

      gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 10                   180                 185                 190

      atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
      Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                      195                 200                 205
 15
      cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
      Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                      210                 215                 220

 20   ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                 230                 235                 240

      ctg tac aag tga                                                   732
 25   Leu Tyr Lys


      <210> 14
      <211> 243
 30   <212> PRT
      <213> Artificial Sequence

      <400> 14
      Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 35    1               5                  10                  15

      Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                      20                  25                  30

 40   Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                      35                  40                  45

      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50                  55                  60
 45
      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65                  70                  75                  80

      Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 50                       85                  90                  95

      Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                      100                 105                 110

 55   Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                      115                 120                 125

      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
             130                 135                 140
 60
      Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                 150                 155                 160

      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 65                   165                 170                 175

      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180                 185                 190

 70   Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                      195                 200                 205
```

```
       Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
          210             215             220

5      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
          225             230             235             240

       Leu Tyr Lys

10
       <210> 15
       <211> 732
       <212> DNA
       <213> Artificial Sequence
15
       <220>
       <223> Description of Artificial Sequence: Arg(CGC)5GFP

       <220>
20     <221> CDS
       <222> (1)..(732)

       <400> 15
       atg cgc cgc cgc cgc cgc agc aag ggc gag gaa ctg ttc act ggc gtg    48
25     Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
         1               5               10                  15

       gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
       Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
30                      20              25                  30

       tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
       Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                   35              40              45
35
       ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
       Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
           50                  55                  60

40     ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
       Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
           65                  70                  75                  80

       gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
45     Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                           85              90                  95

       tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
       Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
50                     100             105             110

       acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
       Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                  115             120             125
55
       gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
       Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
           130             135             140

60     aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
       Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
       145             150             155             160

       aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
65     Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                       165             170             175

       gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
       Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
70                     180             185             190
```

```
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

<210> 16
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 16
```
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

<210> 17

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<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(CGG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 17
atg cgg cgg cgg cgg cgg agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240
```

```
ctg tac aag tga                                          732
Leu Tyr Lys
```

<210> 18
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 18

```
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
               20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
           35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
       50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
   65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                   85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
              100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
          115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
      130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
               165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
              180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
          195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
      210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

<210> 19
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(CGT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 19
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atg cgt cgt cgt cgt cgt agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
         50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

<210> 20
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 20

```
        Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
         1               5                  10                  15

        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                     20                  25                  30

        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                 35                  40                  45

        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50                  55                  60

        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
         65                  70                  75                  80

        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                         85                  90                  95

        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                        100                 105                 110

        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                    115                 120                 125

        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                 135                 140

        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                 150                 155                 160

        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165                 170                 175

        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180                 185                 190

        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195                 200                 205

        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210                 215                 220

        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225                 230                 235                 240

        Leu Tyr Lys


        <210> 21
        <211> 732
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Description of Artificial Sequence: Asn(AAC)5GFP

        <220>
        <221> CDS
        <222> (1)..(732)

        <400> 21
        atg aac aac aac aac aac agc aag ggc gag gaa ctg ttc act ggc gtg    48
        Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
         1               5                  10                  15

        gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                     20                  25                  30

        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
```

```
                35                        40                        45

       ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca      192
       Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
  5        50                        55                        60

       ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca      240
       Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
           65                        70                        75        80
 10
       gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc      288
       Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                       85                        90                        95

 15    tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag      336
       Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                      100                       105                       110

       acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc      384
 20    Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                  115                       120                       125

       gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac      432
       Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 25           130                       135                       140

       aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac      480
       Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
       145                       150                       155                160
 30
       aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att      528
       Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                       170                       175

 35    gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca      576
       Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180                       185                       190

       atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc      624
 40    Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                  195                       200                       205

       cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc      672
       Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 45           210                       215                       220

       ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag      720
       Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
       225                       230                       235                240
 50
       ctg tac aag tga                                                      732
       Leu Tyr Lys
```

```
Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1                   5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60
```

```
        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
         65              70              75              80

 5      Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                         85              90                  95

        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                    100             105             110
10
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                115             120             125

15      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                130             135             140

        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145             150             155             160

20      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165             170             175

        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180             185             190
25
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195             200             205

        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
30          210             215             220

        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225             230             235             240

35      Leu Tyr Lys


        <210> 23
        <211> 732
40      <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Description of Artificial Sequence: Asn(AAT)5GFP
45
        <220>
        <221> CDS
        <222> (1)..(732)

50      <400> 23
        atg aat aat aat aat aat agc aag ggc gag gaa ctg ttc act ggc gtg   48
        Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5              10              15

55      gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                     20              25              30

        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc  144
60      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                 35              40                  45

        ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca  192
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
65          50              55                  60

        ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca  240
        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
          65              70              75              80
70
        gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc  288
```

```
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                     85              90              95

        tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
 5      Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                     100             105             110

        acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
10                   115             120             125

        gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                     130             135             140
15
        aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                 150             155             160

20      aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                     165             170             175

        gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
25      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                     180             185             190

        atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
30                   195             200             205

        cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                     210             215             220
35
        ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225                 230             235             240

40      ctg tac aag tga                                                    732
        Leu Tyr Lys


        <210> 24
45      <211> 243
        <212> PRT
        <213> Artificial Sequence

        <400> 24
50      Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
         1               5               10              15

        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                     20              25              30
55
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                     35              40              45

        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
60           50              55              60

        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
        65              70              75              80

65      Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                     85              90              95

        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                     100             105             110
70
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
```

```
                115                 120                 125

      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
          130                 135                 140
  5
      Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                 150                 155                 160

      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 10                   165                 170                 175

      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                  180                 185                 190
 15
      Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                  195                 200                 205

      Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
          210                 215                 220
 20
      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                 230                 235                 240

      Leu Tyr Lys
 25

      <210> 25
      <211> 732
      <212> DNA
 30   <213> Artificial Sequence

      <220>
      <223> Description of Artificial Sequence: Asp(GAC)5GFP

 35   <220>
      <221> CDS
      <222> (1)..(732)

      <400> 25
 40   atg gac gac gac gac gac agc aag ggc gag gaa ctg ttc act ggc gtg   48
      Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
        1               5                  10                  15

      gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
 45   Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                      20                  25                  30

      tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc  144
      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 50               35                  40                  45

      ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca  192
      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
          50                  55                  60
 55
      ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca  240
      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65                  70                  75                  80

 60   gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc  288
      Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                          85                  90                  95

      tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag  336
 65   Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                      100                 105                 110

      acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc  384
      Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 70               115                 120                 125
```

```
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

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<210> 26
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 26
Met Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1           5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175
```

```
      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
              180                 185                 190

  5   Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
              195                 200                 205

      Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
              210                 215                 220

 10   Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                 230                 235                 240

      Leu Tyr Lys

 15

      <210> 27
      <211> 732
      <212> DNA
      <213> Artificial Sequence
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      <220>
      <223> Description of Artificial Sequence: Asp(GAT)5GFP

      <220>
 25   <221> CDS
      <222> (1)..(732)

      <400> 27
      atg gat gat gat gat gat agc aag ggc gag gaa ctg ttc act ggc gtg    48
 30   Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
       1               5                  10                  15

      gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
 35   Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                  20                  25                  30

      tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
              35                  40                  45
 40
      ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
              50                  55                  60

 45   ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
       65                  70                  75                  80

      gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
 50   Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                          85                  90                  95

      tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
      Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 55                       100                 105                 110

      acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
      Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                  115                 120                 125
 60
      gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
              130                 135                 140

 65   aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
      Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                 150                 155                 160

      aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
 70   Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                          165                 170                 175
```

```
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                     732
Leu Tyr Lys
```

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<210> 28
<211> 243
<212> PRT
<213> Artificial Sequence
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<400> 28
Met Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1           5              10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210             215             220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240
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Leu Tyr Lys

<400> 29

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atg tgc tgc tgc tgc tgc agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc     624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc     672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
```

```
           210                215                220

      ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225             230                 235                240

      ctg tac aag tga                                                    732
      Leu Tyr Lys
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<210> 30
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 30
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Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

<210> 31
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cys(TGT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 31

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atg tgt tgt tgt tgt tgt agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

<210> 32

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<211> 243
<212> PRT
<213> Artificial Sequence

<400> 32
Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys


<210> 33
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gln(CAA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 33
atg caa caa caa caa caa agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
```

```
                 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                          20                  25                  30

  5      tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
         Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                     35                  40                  45

         ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
         Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 10          50                  55                  60

         ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
         Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
         65                  70                  75                  80
 15
         gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
         Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                             85                  90                  95

 20      tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
         Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                         100                 105                 110

         acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
 25      Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                     115                 120                 125

         gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
         Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 30          130                 135                 140

         aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
         Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
         145                 150                 155                 160
 35
         aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
         Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                             165                 170                 175

 40      gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
         Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                         180                 185                 190

         atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
 45      Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                     195                 200                 205

         cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
         Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 50          210                 215                 220

         ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
         Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
         225                 230                 235                 240
 55
         ctg tac aag tga                                                    732
         Leu Tyr Lys

 60      <210> 34
         <211> 243
         <212> PRT
         <213> Artificial Sequence

 65      <400> 34
         Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
           1               5                  10                  15

         Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 70               20                  25                  30
```

```
      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
              35              40                  45
```

```
      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
          50              55                  60
```

```
      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65              70                  75                      80
```

```
      Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                  85                  90                  95
```

```
      Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
              100                 105                 110
```

```
      Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
              115                 120                 125
```

```
      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
              130                 135                 140
```

```
      Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                 150                 155                 160
```

```
      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                  165                 170                 175
```

```
      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                  180                 185                 190
```

```
      Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                  195                 200                 205
```

```
      Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
          210                 215                 220
```

```
      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                 230                 235                 240
```

```
      Leu Tyr Lys
```

```
      <210> 35
      <211> 732
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      <212> DNA
      <213> Artificial Sequence

      <220>
      <223> Description of Artificial Sequence: Gln(CAG)5GFP
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      <220>
      <221> CDS
      <222> (1)..(732)
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      <400> 35
      atg cag cag cag cag cag agc aag ggc gag gaa ctg ttc act ggc gtg    48
      Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
        1               5                  10                  15
```

```
      gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
      Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                  20                  25                  30
```

```
      tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                  35                  40                  45
```

```
      ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
          50              55                  60
```

```
       ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
       Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
        65              70              75              80

 5     gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
       Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85              90              95

10     tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
       Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                    100             105             110

       acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
       Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
15                 115             120             125

       gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
       Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130             135             140
20
       aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
       Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
       145             150             155             160

25     aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
       Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165             170             175

       gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
30     Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                        180             185             190

       atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
       Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
35                 195             200             205

       cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
       Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                    210             215             220
40
       ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
       Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
       225             230             235             240

45     ctg tac aag tga                                                    732
       Leu Tyr Lys


       <210> 36
50     <211> 243
       <212> PRT
       <213> Artificial Sequence

       <400> 36
55     Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
        1               5               10              15

       Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                    20              25              30
60
       Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35              40              45

       Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
65          50              55              60

       Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
        65              70              75              80

70     Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85              90              95
```

```
       Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                   100                 105                 110

 5     Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                   115                 120                 125

       Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                   130                 135                 140
10
       Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
       145                 150                 155                 160

       Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
15                     165                 170                 175

       Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                   180                 185                 190

20     Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                   195                 200                 205

       Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                   210                 215                 220
25
       Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
       225                 230                 235                 240

       Leu Tyr Lys
30


       <210> 37
       <211> 732
       <212> DNA
35     <213> Artificial Sequence

       <220>
       <223> Description of Artificial Sequence: Gly(GAA)5GFP

40     <220>
       <221> CDS
       <222> (1)..(732)

       <400> 37
45     atg gaa gaa gaa gaa gaa agc aag ggc gag gaa ctg ttc act ggc gtg    48
       Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
         1               5                  10                  15

       gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
50     Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                       20                  25                  30

       tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
       Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
55                 35                  40                  45

       ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
       Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50                  55                  60
60
       ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
       Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
         65                  70                  75                  80

65     gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
       Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                           85                  90                  95

       tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
70     Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                   100                 105                 110
```

```
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 38
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 38
Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
```

```
           145                150                155                160
      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
5                     165                170                175
      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180                185                190
      Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
10                    195                200                205
      Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                  210                215                220
15    Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                230                235                240

      Leu Tyr Lys
20
      <210> 39
      <211> 732
      <212> DNA
      <213> Artificial Sequence
25
      <220>
      <223> Description of Artificial Sequence: Glu(GAG)5GFP

      <220>
30    <221> CDS
      <222> (1)..(732)

      <400> 39
      atg gag gag gag gag gag agc aag ggc gag gaa ctg ttc act ggc gtg   48
35    Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
        1               5                10                15

      gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
      Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
40                   20                25                30

      tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc  144
      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                 35                40                45
45
      ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca  192
      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
           50                55                60

50    ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca  240
      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
       65                70                75                80

      gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc  288
55    Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                         85                90                95

      tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag  336
      Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
60                   100               105               110

      acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc  384
      Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
               115               120               125
65
      gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac  432
      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
           130               135               140

70    aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac  480
      Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
```

```
            145                150                155                160

      aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
 5                    165                170                175

      gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180                185                190
10
      atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
      Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                      195                200                205
15
      cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
      Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                      210                215                220

      ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
20    225                230                235                240

      ctg tac aag tga                                                    732
      Leu Tyr Lys
25


      <210> 40
      <211> 243
      <212> PRT
30    <213> Artificial Sequence

      <400> 40
      Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
        1               5                  10                 15
35
      Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                      20                 25                 30

      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
40                 35                 40                 45

      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                 50                 55                 60

45    Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
        65                 70                 75                 80

      Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                          85                 90                 95
50
      Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                      100                105                110

      Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
55               115                120                125

      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
               130                135                140

60    Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                150                155                160

      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                170                175
65
      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180                185                190

      Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
70                 195                200                205
```

```
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210             215             220

 5      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225             230             235             240

        Leu Tyr Lys


10      <210> 41
        <211> 732
        <212> DNA
        <213> Artificial Sequence

15      <220>
        <223> Description of Artificial Sequence: Gly(GGA)5GFP

        <220>
        <221> CDS
20      <222> (1)..(732)

        <400> 41
        atg gga gga gga gga gga agc aag ggc gag gaa ctg ttc act ggc gtg    48
        Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
25       1           5               10              15

        gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                    20              25              30
30
        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                35              40              45

35      ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
            50              55              60

        ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
40      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
            65              70              75              80

        gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
45                      85              90              95

        tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                    100             105             110
50
        acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                115             120             125

55      gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130             135             140

        aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
60      Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145             150             155             160

        aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
65                      165             170             175

        gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180             185             190
70
        atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
```

```
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
             195                 200                 205
```

```
        cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
             210                 215                 220
```

```
        ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225                 230                 235                 240
```

```
        ctg tac aag tga                                                   732
        Leu Tyr Lys
```

```
        <210> 42
        <211> 243
        <212> PRT
        <213> Artificial Sequence
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```
        <400> 42
        Met Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5                10                15
```

```
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                     20                 25                 30
```

```
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                 35                 40                 45
```

```
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50                 55                 60
```

```
        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
        65                 70                 75                 80
```

```
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                         85                 90                 95
```

```
        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                     100                105                110
```

```
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                 115                120                125
```

```
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
             130                135                140
```

```
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                150                155                160
```

```
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                     165                170                175
```

```
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                 180                185                190
```

```
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
             195                 200                 205
```

```
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
             210                 215                 220
```

```
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225                 230                 235                 240
```

```
        Leu Tyr Lys
```

```
        <210> 43
        <211> 732
```

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 43

```
atg ggc ggc ggc ggc agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc  144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca  192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca  240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc  288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag  336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc  384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac  432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac  480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att  528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca  576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc  624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc  672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag  720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240
```

```
ctg tac aag tga                                                           732
Leu Tyr Lys
```

<210> 44
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 44

```
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

<210> 45
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 45

```
atg ggg ggg ggg ggg ggg agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
         115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
     130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
             180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
             195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
         210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 46
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 46
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
```

```
        1               5                    10                      15

        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
5                20                    25                      30

        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35                    40                    45
10
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                50                    55                    60

        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
        65                    70                    75                    80
15
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                          85                    90                    95

        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                        100                   105                   110
20
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                    115                   120                   125

        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
25          130                   135                   140

        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                   150                   155                   160
30
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165                   170                   175

        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                        180                   185                   190
35
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195                   200                   205

        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
40          210                   215                   220

        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225                   230                   235                   240

45      Leu Tyr Lys


        <210> 47
        <211> 732
50      <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Description of Artificial Sequence: Gly(GGT)5GFP
55
        <220>
        <221> CDS
        <222> (1)..(732)

60      <400> 47
        atg ggt ggt ggt ggt ggt agc aag ggc gag gaa ctg ttc act ggc gtg    48
        Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5                    10                      15

65      gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                        20                    25                      30

        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
70      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35                    40                    45
```

```
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65              70              75              80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85              90              95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 48
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 48
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60
```

```
          Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
              65              70              75              80

      5   Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                          85              90              95

          Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                      100             105             110

     10   Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                      115             120             125

          Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                  130             135             140

     15   Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
              145             150             155             160

          Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
     20                   165             170             175

          Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180             185             190

     25   Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                      195             200             205

          Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                  210             215             220

     30   Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
          225             230             235             240

          Leu Tyr Lys
     35
```

<210> 49
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: His(CAC)5GFP

<220>
<221> CDS
<222> (1)..(732)

```
<400> 49
atg cac cac cac cac cac agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
              20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
          35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
      50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
  65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
```

```
                        85                    90                    95
     tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
5    Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                 100               105               110

     acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
     Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                 115               120               125
10
     gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
     Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
             130               135               140

15   aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
     Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
     145               150               155               160

     aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
20   Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                 165               170               175

     gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
     Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
25               180               185               190

     atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
     Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                 195               200               205
30
     cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
     Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
             210               215               220

35   ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
     Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
     225               230               235               240

     ctg tac aag tga                                                   732
40   Leu Tyr Lys


     <210> 50
     <211> 243
45   <212> PRT
     <213> Artificial Sequence

     <400> 50
     Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
50    1               5                10                15

     Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                 20                25                30

55   Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                 35                40                45

     Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
         50                55                60
60
     Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
     65                70                75                80

     Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
65                   85                90                95

     Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                 100               105               110

70   Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
             115               120               125
```

```
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                 135                 140

        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                 150                 155                 160

        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165                 170                 175

        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180                 185                 190

        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195                 200                 205

        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210                 215                 220

        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225                 230                 235                 240

        Leu Tyr Lys


        <210> 51
        <211> 732
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Description of Artificial Sequence: His(CAT)5GFP

        <220>
        <221> CDS
        <222> (1)..(732)

        <400> 51
        atg cat cat cat cat cat agc aag ggc gag gaa ctg ttc act ggc gtg    48
        Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5                  10                  15

        gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                        20                  25                  30

        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35                  40                  45

        ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
            50                  55                  60

        ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
        65                  70                  75                  80

        gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85                  90                  95

        tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                        100                 105                 110

        acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                    115                 120                 125

        gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
```

```
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130             135             140

  5     aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145             150             155             160

        aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
 10     Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165             170             175

        gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180             185             190
 15
        atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195             200             205

 20     cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                    210             215             220

        ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
 25     Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225             230             235             240

        ctg tac aag tga                                                    732
        Leu Tyr Lys
 30


        <210> 52
        <211> 243
        <212> PRT
 35     <213> Artificial Sequence

        <400> 52
        Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
            1               5               10              15
 40
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                    20              25              30

        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 45                 35              40              45

        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
            50              55              60

 50     Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
            65              70              75              80

        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85              90              95
 55
        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                    100             105             110

        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 60                 115             120             125

        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130             135             140

 65     Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
            145             150             155             160

        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165             170             175
 70
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
```

```
                180                    185                    190
     Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
             195                 200                 205
 5
     Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
             210                 215                 220

     Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
10   225                 230                 235                 240

     Leu Tyr Lys
```

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15   <210> 53
     <211> 732
     <212> DNA
     <213> Artificial Sequence

20   <220>
     <223> Description of Artificial Sequence: Ile(ATA)5GFP

     <220>
     <221> CDS
25   <222> (1)..(732)

     <400> 53
     atg ata ata ata ata ata agc aag ggc gag gaa ctg ttc act ggc gtg    48
     Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
30    1               5                  10                  15

     gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
     Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                  20                  25                  30
35
     tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
     Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                  35                  40                  45

40   ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
     Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
          50                  55                  60

     ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
45   Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65                  70                  75                  80

     gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
     Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
50                       85                  90                  95

     tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
     Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                 100                 105                 110
55
     acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
     Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
             115                 120                 125

60   gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
     Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
             130                 135                 140

     aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
65   Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
     145                 150                 155                 160

     aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
     Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
70                      165                 170                 175
```

```
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
        180             185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210             215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

<210> 54
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 54
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Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240
```

Leu Tyr Lys

<210> 55
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 55

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atg atc atc atc atc atc agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
               100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
           115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
       130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
               165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
           180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
           195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
       210                 215                 220
```

```
        ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225             230             235             240
  5
        ctg tac aag tga                                                    732
        Leu Tyr Lys
```

 10   <210> 56
        <211> 243
        <212> PRT
        <213> Artificial Sequence

 15   <400> 56
        Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1   5   10   15

        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 20   20   25   30

        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35   40   45

 25   Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                50   55   60

        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
         65   70   75   80
 30
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85   90   95

        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
 35   100   105   110

        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                    115   120   125

 40   Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                130   135   140

        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145   150   155   160
 45
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165   170   175

        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 50   180   185   190

        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195   200   205

 55   Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                210   215   220

        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225   230   235   240
 60
        Leu Tyr Lys

        <210> 57
 65   <211> 732
        <212> DNA
        <213> Artificial Sequence

        <220>
 70   <223> Description of Artificial Sequence: Ile(ATT)5GFP
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<220>
<221> CDS
<222> (1)..(732)

<400> 57
atg att att att att att agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                    85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc     624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc     672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag     720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                      732
Leu Tyr Lys

<210> 58
<211> 243
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```
<212> PRT
<213> Artificial Sequence

<400> 58
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys


<210> 59
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 59
atg cta cta cta cta cta agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
```

```
                     20                  25                  30

        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
5               35                  40                  45

        ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                50                  55                  60
10

        ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
        65                  70                  75                  80

15      gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85                  90                  95

        tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
20      Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                        100                 105                 110

        acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
25                      115                 120                 125

        gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                130                 135                 140
30

        aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                 150                 155                 160

35      aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165                 170                 175

        gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
40      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                        180                 185                 190

        atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
45                      195                 200                 205

        cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                210                 215                 220
50

        ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225                 230                 235                 240

55                                                                        732
        ctg tac aag tga
        Leu Tyr Lys
```

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<210> 60
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 60
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
```

```
                 35                    40                     45
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
            50                  55                  60
        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
            65                  70                  75                  80
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85                  90                  95
        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                    100                 105                 110
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                115                 120                 125
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                 135                 140
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                 150                 155                 160
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165                 170                 175
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                        180                 185                 190
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195                 200                 205
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210                 215                 220
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225                 230                 235                 240
        Leu Tyr Lys


        <210> 61
        <211> 732
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Description of Artificial Sequence: Leu(CTC)5GFP

        <220>
        <221> CDS
        <222> (1)..(732)

        <400> 61
        atg ctc ctc ctc ctc ctc agc aag ggc gag gaa ctg ttc act ggc gtg    48
        Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5                   10                  15

        gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                    20                  25                  30

        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                35                  40                  45

        ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
            50                  55                  60

        ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
```

```
      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65              70              75              80
```

```
 5    gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
      Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                      85              90              95
```

```
      tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
10    Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                      100             105             110
```

```
      acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
      Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                  115             120             125
15
```

```
      gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
20    Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
              130             135             140
```

```
      aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
      Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145             150             155             160
```

```
25    aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165             170             175
```

```
      gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
30    Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                  180             185             190
```

```
      atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
      Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                  195             200             205
35
```

```
      cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
40    Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
              210             215             220
```

```
      ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225             230             235             240
```

```
      ctg tac aag tga                                                    732
45    Leu Tyr Lys
```

```
      <210> 62
      <211> 243
50    <212> PRT
      <213> Artificial Sequence
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```
      <400> 62
      Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
55    1               5               10              15
```

```
      Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
60                  20              25              30
```

```
      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                  35              40              45
```

```
      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
              50              55              60
65
```

```
      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65              70              75              80
```

```
      Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
70                  85              90              95
```

```
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
        100             105         110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120         125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135         140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150         155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165         170             175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180         185         190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195         200         205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215         220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230         235             240

Leu Tyr Lys
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<210> 63
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 63
atg ctg ctg ctg ctg ctg agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1           5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110
```

```
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                     732
Leu Tyr Lys
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<210> 64
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 64
Met Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160
```

```
                    Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                                    165             170             175

    5               Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                                180             185             190

                    Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                                195             200             205
   10
                    Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                                210             215             220

                    Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
   15               225             230             235             240

                    Leu Tyr Lys


   20               <210> 65
                    <211> 732
                    <212> DNA
                    <213> Artificial Sequence

   25               <220>
                    <223> Description of Artificial Sequence: Leu(CTT)5GFP

                    <220>
                    <221> CDS
   30               <222> (1)..(732)

                    <400> 65
                    atg ctt ctt ctt ctt ctt agc aag ggc gag gaa ctg ttc act ggc gtg   48
   35               Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
                     1               5              10              15

                    gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
                    Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                                    20              25              30
   40
                    tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
                    Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                                35              40              45

   45               ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
                    Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                        50              55              60

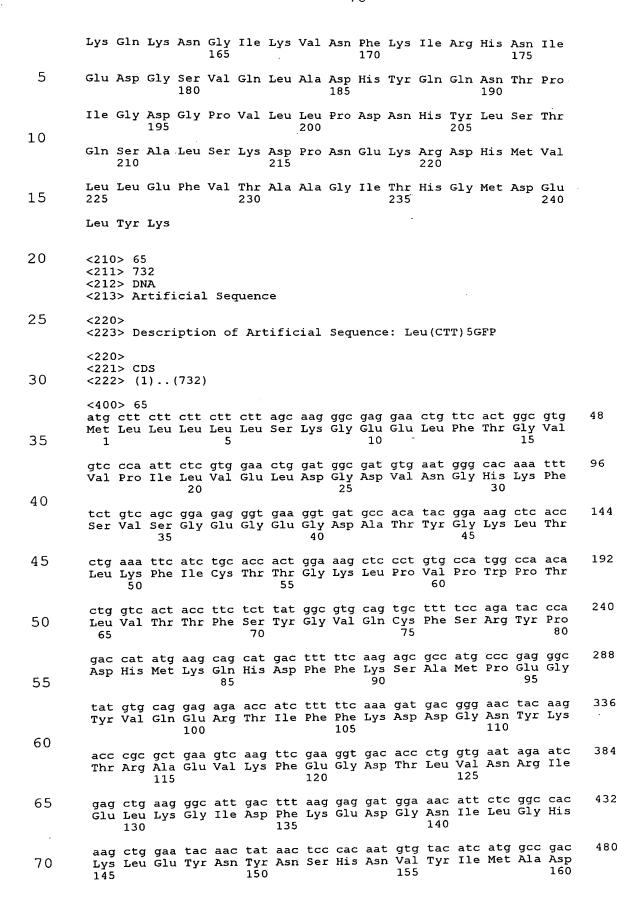                    ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
   50               Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
                    65              70              75              80

                    gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
                    Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
   55                               85              90              95

                    tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
                    Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                                    100             105             110
   60
                    acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
                    Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                                115             120             125

   65               gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
                    Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                        130             135             140

                    aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
   70               Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
                    145             150             155             160
```

```
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
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<210> 66
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 66

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Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
```

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                210                 215                 220
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
5       225                 230                 235                 240

        Leu Tyr Lys


        <210> 67
10      <211> 732
        <212> DNA
        <213> Artificial Sequence

        <220>
15      <223> Description of Artificial Sequence: Leu(TTA)5GFP

        <220>
        <221> CDS
        <222> (1)..(732)
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        <400> 67
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        Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
         1               5                   10                  15
25
        gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                     20                  25                  30

30      tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                 35                  40                  45

        ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
35      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50                  55                  60

        ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
40       65                  70                  75                  80

        gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                         85                  90                  95
45
        tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                     100                 105                 110

50      acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                     115                 120                 125

        gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
55      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                 130                 135                 140

        aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
60      145                 150                 155                 160

        aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                         165                 170                 175
65
        gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                     180                 185                 190

70      atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
```

```
                195                    200                    205
        cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc  672
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
  5         210             215                 220

        ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag  720
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225             230                 235                 240
 10
        ctg tac aag tga                                                   732
        Leu Tyr Lys
```

15   <210> 68
      <211> 243
      <212> PRT
      <213> Artificial Sequence

20   <400> 68

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      Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
        1               5                   10                  15

      Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                    20                  25                  30

      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                35                  40                  45

      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
            50                  55                  60

      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
        65                  70                  75                  80

      Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85                  90                  95

      Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                    100                 105                 110

      Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                115                 120                 125

      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                 135                 140

      Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                 150                 155                 160

      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165                 170                 175

      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180                 185                 190

      Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195                 200                 205

      Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                210                 215                 220

      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                 230                 235                 240

      Leu Tyr Lys
```

70   <210> 69
      <211> 732
      <212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(TTG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 69

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atg ttg ttg ttg ttg ttg agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc     624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc     672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag     720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                      732
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Leu Tyr Lys

<210> 70
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 70
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Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
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<210> 71
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Lys(AAA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 71
atg aaa aaa aaa aaa aaa agc aag ggc gag gaa ctg ttc act ggc gtg   48

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        Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5                   10                  15

  5     gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                         20                  25                  30

        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
 10                      35                  40                  45

        ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                50                  55                  60
 15
        ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
        65                  70                  75                  80

 20     gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                         85                  90                  95

        tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
 25     Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                         100                 105                 110

        acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
 30                      115                 120                 125

        gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                130                 135                 140
 35
        aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                 150                 155                 160

 40     aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                         165                 170                 175

        gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
 45     Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                         180                 185                 190

        atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
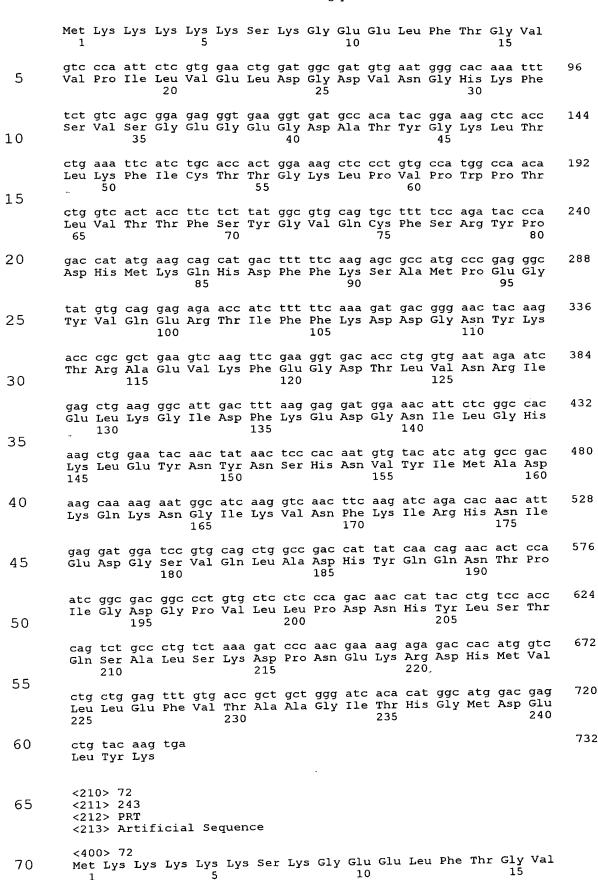 50                      195                 200                 205

        cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                210                 215                 220
 55
        ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225                 230                 235                 240

 60     ctg tac aag tga                                                   732
        Leu Tyr Lys


        <210> 72
 65     <211> 243
        <212> PRT
        <213> Artificial Sequence

        <400> 72
 70     Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5                   10                  15
```

```
          Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                      20              25                  30
 5        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                      35              40                  45

          Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                  50              55              60
10        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
              65              70              75                      80

          Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
15                        85              90                  95

          Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                      100             105                 110
20        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                      115             120                 125

          Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                  130             135                 140
25        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
          145                 150                 155                 160

          Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
30                            165             170                 175

          Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                          180             185                 190
35        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                      195             200                 205

          Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                      210             215                 220
40        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
          225                 230                 235                 240

          Leu Tyr Lys
45

          <210> 73
          <211> 732
          <212> DNA
50        <213> Artificial Sequence

          <220>
          <223> Description of Artificial Sequence: Lys(AAG)5GFP

55        <220>
          <221> CDS
          <222> (1)..(732)

          <400> 73
60        atg aag aag aag aag aag agc aag ggc gag gaa ctg ttc act ggc gtg    48
          Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
            1               5                  10                  15

          gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
65        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                      20                  25                  30

          tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
          Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
70                    35                  40                  45
```

```
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

<210> 74
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 74

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Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
```

```
        65                    70                    75                    80

        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                          85                    90                    95
 5
        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                        100                   105                   110

        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
10                  115                   120                   125

        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                130                   135                   140
15
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145               150                   155                   160

        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165                   170                   175
20
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                        180                   185                   190

        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
25                  195                   200                   205

        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                210                   215                   220
30
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225               230                   235                   240

        Leu Tyr Lys
35
        <210> 75
        <211> 732
        <212> DNA
        <213> Artificial Sequence
40
        <220>
        <223> Description of Artificial Sequence: Phe(CTT)5GFP

        <220>
45      <221> CDS
        <222> (1)..(732)

        <400> 75
        atg ttg ttg ttg ttg ttg agc aag ggc gag gaa ctg ttc act ggc gtg    48
50      Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5                   10                  15

        gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
55                      20                  25                  30

        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35                  40                  45
60
        ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                50                  55                  60

65      ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
          65                  70                  75                  80

        gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
70      Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                          85                  90                  95
```

```
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115             120             125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 76
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 76
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125
```

```
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130             135             140

 5      Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145             150             155             160

        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                    165             170             175

10      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180             185             190

        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195             200             205

15      Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                    210             215             220

20      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225             230             235             240

        Leu Tyr Lys


25      <210> 77
        <211> 732
        <212> DNA
        <213> Artificial Sequence

30      <220>
        <223> Description of Artificial Sequence: Phe(TTC)5GFP

        <220>
        <221> CDS
35      <222> (1)..(732)

        <400> 77
        atg ttc ttc ttc ttc ttc agc aag ggc gag gaa ctg ttc act ggc gtg    48
        Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
40        1               5                  10                  15

        gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                     20                  25                  30
45
        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                 35                  40                  45

50      ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50                  55                  60

        ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
55      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
         65                  70                  75                  80

        gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
60                      85                  90                  95

        tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                    100             105             110
65
        acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                115             120             125

70      gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
```

```
              130                    135                    140
  5     aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                 150                 155                 160

 10     aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165                 170                 175

        gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                        180                 185                 190

 15     atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                        195                 200                 205

 20     cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                210                 215                 220

        ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 25     225                 230                 235                 240

        ctg tac aag tga                                                   732
        Leu Tyr Lys

 30
        <210> 78
        <211> 243
        <212> PRT
        <213> Artificial Sequence
 35
        <400> 78
        Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5                  10                  15

 40     Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                        20                  25                  30

        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35                  40                  45

 45     Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                50                  55                  60

        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 50     65                  70                  75                  80

        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85                  90                  95

 55     Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                        100                 105                 110

        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                    115                 120                 125

 60     Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                130                 135                 140

        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 65     145                 150                 155                 160

        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165                 170                 175

 70     Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                        180                 185                 190
```

```
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

Leu Tyr Lys
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<210> 79
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CCC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 79
atg ccc ccc ccc ccc ccc agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
```

```
     Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                 180                 185                 190

 5   atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
     Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                 195                 200                 205

     cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
10   Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                 210                 215                 220

     ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
     Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
     225                 230                 235                 240
15
     ctg tac aag tga                                                    732
     Leu Tyr Lys


20   <210> 80
     <211> 243
     <212> PRT
     <213> Artificial Sequence

25   <400> 80
     Met Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
       1               5                 10                  15

     Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
30                   20                  25                  30

     Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                 35                  40                  45

35   Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
           50                  55                  60

     Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
     65                  70                  75                  80
40
     Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                     85                  90                  95

     Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
45                   100                 105                 110

     Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                 115                 120                 125

50   Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                 130                 135                 140

     Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
     145                 150                 155                 160
55
     Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                     165                 170                 175

     Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
60                   180                 185                 190

     Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                 195                 200                 205

65   Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                 210                 215                 220

     Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
     225                 230                 235                 240
70
     Leu Tyr Lys
```

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<210> 81
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CCG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 81
atg ccg ccg ccg ccg ccg agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc     624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc     672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220
```

```
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240
```

5
```
ctg tac aag tga                                                    732
Leu Tyr Lys
```

10
```
<210> 82
<211> 243
<212> PRT
<213> Artificial Sequence
```

15
```
<400> 82
Met Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5               10              15
```

20
```
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30
```

```
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35              40              45
```

25
```
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60
```

```
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80
```

30
```
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85              90              95
```

```
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110
```

35
```
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115             120             125
```

```
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130             135             140
```

40
```
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160
```

45
```
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175
```

```
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190
```

50
```
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200             205
```

```
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210             215             220
```

55
```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240
```

60
```
Leu Tyr Lys
```

65
```
<210> 83
<211> 732
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Pro(CCT)5GFP
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70
```
<220>
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<221> CDS
<222> (1)..(732)

<400> 83

```
atg cct cct cct cct cct agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
         50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc     624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc     672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag     720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                     732
Leu Tyr Lys
```

<210> 84
<211> 243
<212> PRT

<213> Artificial Sequence

<400> 84

```
Met Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1           5              10                 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
        100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
        180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

Leu Tyr Lys
```

<210> 85
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CGA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 85

```
atg cga cga cga cga agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1           5              10                 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt  96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30
```

```
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys


<210> 86
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 86
Met Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45
```

```
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55              60
```

5
```
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65                  70              75                  80
```

```
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85              90              95
```
10

```
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100             105             110
```

```
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115             120             125
```
15

```
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140
```

```
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160
```
20

```
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175
```

25
```
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180             185             190
```

```
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195             200             205
```
30

```
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220
```

35
```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240
```

```
Leu Tyr Lys
```

40

```
<210> 87
<211> 732
<212> DNA
<213> Artificial Sequence
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45
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<220>
<223> Description of Artificial Sequence: Ser(AGC)5GFP
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```
<220>
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50
```
<221> CDS
<222> (1)..(732)
```

```
<400> 87
atg agc agc agc agc agc agc aag ggc gag gaa ctg ttc act ggc gtg    48
```
55
```
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5               10              15
```

```
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
```
60
```
                20              25              30
```

```
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
```
65
```
            35              40              45
```

```
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55              60
```
70

```
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
```

```
                65                    70                    75                    80

    5      gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
           Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                            85                    90                    95

           tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
           Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
   10                       100                   105                   110

           acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
           Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                        115                   120                   125

   15      gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
           Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                130                   135                   140

   20      aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
           Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
           145                   150                   155                   160

           aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
           Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
   25                       165                   170                   175

           gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
           Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
   30                       180                   185                   190

           atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc     624
           Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                        195                   200                   205

   35      cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc     672
           Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                210                   215                   220

   40      ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag     720
           Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
           225                   230                   235                   240

           ctg tac aag tga                                                     732
           Leu Tyr Lys
   45


   50      <210> 88
           <211> 243
           <212> PRT
           <213> Artificial Sequence

           <400> 88
           Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
   55       1               5                   10                  15

           Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                        20                  25                  30

   60      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                        35                  40                  45

           Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                50                  55                  60

   65      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
                65                  70                  75                  80

           Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                            85                  90                  95
   70
           Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
```

```
                    100                      105                      110

       Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
               115                  120                  125
  5
       Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
               130                  135                  140

       Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 10    145                  150                  155                  160

       Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                   165                  170                  175
 15    Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                   180                  185                  190

       Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
               195                  200                  205
 20
       Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
               210                  215                  220

       Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 25    225                  230                  235                  240

       Leu Tyr Lys


 30    <210> 89
       <211> 732
       <212> DNA
       <213> Artificial Sequence

 35    <220>
       <223> Description of Artificial Sequence: Ser(AGT)5GFP

       <220>
       <221> CDS
 40    <222> (1)..(732)

       <400> 89
       atg agt agt agt agt agt agc aag ggc gag gaa ctg ttc act ggc gtg    48
       Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 45      1               5                  10                  15

       gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
       Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                        20                  25                  30
 50
       tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
       Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35                  40                  45

 55    ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
       Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
               50                  55                  60

       ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
 60    Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
         65                  70                  75                  80

       gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
       Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 65                      85                  90                  95

       tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
       Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                       100                 105                 110
 70
       acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
```

```
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120             125

  5     gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                 135             140

        aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 10     145                 150             155                 160

        aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165             170             175
 15

        gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180             185             190

 20     atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195             200             205

        cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
 25     Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210                 215             220

        ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 30     225                 230             235                 240

        ctg tac aag tga                                                   732
        Leu Tyr Lys
 35

        <210> 90
        <211> 243
        <212> PRT
        <213> Artificial Sequence
 40
        <400> 90
        Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5               10              15

 45     Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                        20              25              30

        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35              40              45
 50
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
            50              55              60

        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 55     65              70              75              80

        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85              90              95

 60     Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                    100             105             110

        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120             125
 65
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                 135             140

        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 70     145                 150             155                 160
```

```
         Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                     165             170             175

 5       Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                     180             185             190

         Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                     195             200             205

10       Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                 210             215             220

         Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
         225             230             235             240

15
         Leu Tyr Lys


         <210> 91
20       <211> 732
         <212> DNA
         <213> Artificial Sequence

         <220>
25       <223> Description of Artificial Sequence: Ser(TCA)5GFP

         <220>
         <221> CDS
         <222> (1)..(732)
30
         <400> 91
         atg tca tca tca tca tca agc aag ggc gag gaa ctg ttc act ggc gtg    48
         Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5                  10                  15
35
         gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
         Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                         20                  25                  30

40       tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
         Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                     35                  40                  45

         ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
45       Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50                  55                  60

         ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
50       Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
         65                  70                  75                  80

         gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
         Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                         85                  90                  95
55
         tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
         Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                         100             105             110

60       acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
         Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                     115             120             125

         gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
65       Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                     130             135             140

         aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
         Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
70       145             150             155             160
```

```
    aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
    Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                    165                 170                 175

5   gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
    Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180                 185                 190

10  atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
    Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195                 200                 205

    cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
    Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
15                  210                 215                 220

    ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
    Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
    225                 230                 235                 240
20

    ctg tac aag tga                                                    732
    Leu Tyr Lys


25  <210> 92
    <211> 243
    <212> PRT
    <213> Artificial Sequence

30  <400> 92
    Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
      1               5                  10                  15

    Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
35                  20                  25                  30

    Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35                  40                  45

40  Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
              50                  55                  60

    Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65                  70                  75                  80
45
    Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                    85                  90                  95

    Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
50                  100                 105                 110

    Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                    115                 120                 125

55  Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
              130                 135                 140

    Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
    145                 150                 155                 160
60
    Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                    165                 170                 175

    Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
65                  180                 185                 190

    Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195                 200                 205

70  Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                    210                 215                 220
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        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225             230             235             240

  5     Leu Tyr Lys


        <210> 93
        <211> 732
 10     <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Description of Artificial Sequence: Ser(TCC)5GFP
 15
        <220>
        <221> CDS
        <222> (1)..(732)

 20     <400> 93
        atg tcc tcc tcc tcc tcc agc aag ggc gag gaa ctg ttc act ggc gtg    48
        Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5                  10                  15

 25     gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                       20                  25                  30

        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
 30     Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                   35                  40                  45

        ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 35          50                  55                  60

        ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
         65                  70                  75                  80
 40
        gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                            85                  90                  95

 45     tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                       100                 105                 110

        acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
 50     Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                   115                 120                 125

        gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 55          130                 135                 140

        aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                 150                 155                 160
 60
        aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                           165                 170                 175

 65     gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                       180                 185                 190

        atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
 70     Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                       195                 200                 205
```

```
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                    732
Leu Tyr Lys
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<210> 94
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 94

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Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
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<210> 95
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ser(TCG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 95

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atg tcg tcg tcg tcg tcg agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                   732
Leu Tyr Lys
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<210> 96
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 96
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
             100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
         115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
     130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                 165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
             180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
         195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
     210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys


<210> 97
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ser(TCT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 97
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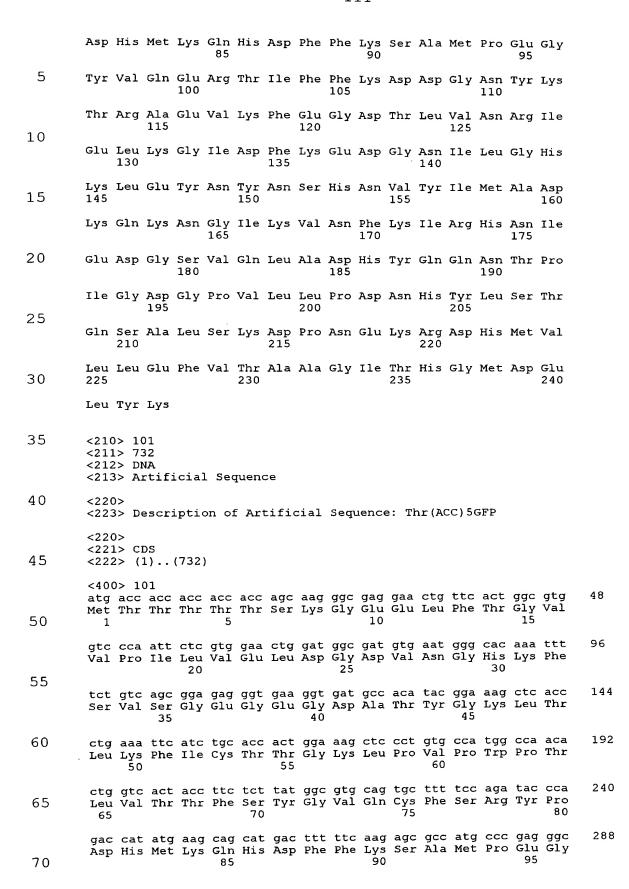Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
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          1               5               10              15

     gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
     Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
              20              25              30

     tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
     Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
              35              40              45

     ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
     Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
              50              55              60

     ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
     Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
     65              70              75              80

     gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
     Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                  85              90              95

     tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
     Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                  100             105             110

     acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
     Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
              115             120             125

     gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
     Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
              130             135             140

     aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
     Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
     145             150             155             160

     aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
     Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                  165             170             175

     gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
     Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
              180             185             190

     atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
     Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
              195             200             205

     cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
     Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
              210             215             220

     ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
     Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
     225             230             235             240

     ctg tac aag tga                                                    732
     Leu Tyr Lys


     <210> 98
     <211> 243
     <212> PRT
     <213> Artificial Sequence

     <400> 98
     Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
     1               5               10              15
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        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                    20                  25                  30

   5    Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35                  40                  45

        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
              50                  55                  60

  10    Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
              65                  70                  75                  80

        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                          85                  90                  95
  15
        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                        100                 105                 110

  20    Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                    115                 120                 125

        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
              130                 135                 140

  25    Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                 150                 155                 160

        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165                 170                 175
  30
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180                 185                 190

        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
  35                195                 200                 205

        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
              210                 215                 220

  40    Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225                 230                 235                 240

        Leu Tyr Lys

  45
        <210> 99
        <211> 732
        <212> DNA
        <213> Artificial Sequence
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        <220>
        <223> Description of Artificial Sequence: Thr(ACA)5GFP

        <220>
  55    <221> CDS
        <222> (1)..(732)

        <400> 99
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        Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  60     1               5                  10                  15

        gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
  65                20                  25                  30

        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35                  40                  45
  70
        ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
```

```
      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
          50                  55                  60

 5    ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
          65                  70                  75                  80

      gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
      Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
10                        85                  90                  95

      tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
      Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                      100                 105                 110
15
      acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
      Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                  115                 120                 125

20    gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
              130                 135                 140

      aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
25    Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                 150                 155                 160

      aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
30                        165                 170                 175

      gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180                 185                 190

35
      atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc     624
      Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                  195                 200                 205

40    cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc     672
      Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
              210                 215                 220

      ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag     720
45    Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                 230                 235                 240

      ctg tac aag tga                                                     732
      Leu Tyr Lys
50

      <210> 100
      <211> 243
      <212> PRT
55    <213> Artificial Sequence

      <400> 100
      Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
        1               5                   10                  15
60
      Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                      20                  25                  30

      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
65                    35                  40                  45

      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
          50                  55                  60

70    Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
          65                  70                  75                  80
```

```
          Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                              85              90                  95

  5       Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                      100             105                 110

          Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                      115             120                 125
 10
          Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
              130             135                 140

          Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 15       145             150                 155                 160

          Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165             170                 175

 20       Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                      180             185                 190

          Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                      195             200                 205
 25
          Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
              210             215                 220

          Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 30       225             230                 235                 240

          Leu Tyr Lys
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 35       <210> 101
          <211> 732
          <212> DNA
          <213> Artificial Sequence

 40       <220>
          <223> Description of Artificial Sequence: Thr(ACC)5GFP

          <220>
          <221> CDS
 45       <222> (1)..(732)

          <400> 101
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          Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 50        1               5                  10                  15

          gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
          Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                          20                  25                  30
 55
          tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
          Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                      35                  40                  45

 60       ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
          Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
              50                  55                  60

          ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
 65       Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
              65                  70                  75                  80

          gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
          Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
 70                       85                  90                  95
```

```
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys


<210> 102
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 102
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1                   5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
```

```
            130                    135                    140
     Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
     145                 150                 155                 160

     Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                     165                 170                 175

     Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                     180                 185                 190

     Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                 195                 200                 205

     Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                 210                 215                 220

     Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
     225                 230                 235                 240

     Leu Tyr Lys


     <210> 103
     <211> 732
     <212> DNA
     <213> Artificial Sequence

     <220>
     <223> Description of Artificial Sequence: Thr(ACG)5GFP

     <220>
     <221> CDS
     <222> (1)..(732)

     <400> 103
     atg acg acg acg acg acg agc aag ggc gag gaa ctg ttc act ggc gtg    48
     Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
       1           5                  10                  15

     gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
     Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                 20                  25                  30

     tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
     Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                 35                  40                  45

     ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
     Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50                  55                  60

     ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
     Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
     65                  70                  75                  80

     gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
     Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                     85                  90                  95

     tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
     Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                 100                 105                 110

     acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
     Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                 115                 120                 125

     gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
     Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                 130                 135                 140
```

```
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                   732
Leu Tyr Lys


<210> 104
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 104
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190
```

```
      Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
              195                 200                 205

 5    Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
              210                 215                 220

      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                 230                 235                 240

10    Leu Tyr Lys
```

```
      <210> 105
      <211> 732
15    <212> DNA
      <213> Artificial Sequence

      <220>
      <223> Description of Artificial Sequence: Thr(ACT)5GFP
20
      <220>
      <221> CDS
      <222> (1)..(732)

25    <400> 105
      atg act act act act act agc aag ggc gag gaa ctg ttc act ggc gtg     48
      Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
       1               5                  10                  15

30    gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt     96
      Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                      20                  25                  30

      tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
35    Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                  35                  40                  45

      ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
      Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
40        50                  55                  60

      ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
      Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
      65                  70                  75                  80
45
      gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
      Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                      85                  90                  95

50    tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
      Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                      100                 105                 110

      acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
55    Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                  115                 120                 125

      gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
      Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
60        130                 135                 140

      aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
      Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
      145                 150                 155                 160
65
      aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
      Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                 170                 175

70    gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
      Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
```

		180					185						190		

```
                180                   185                       190

     atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc  624
     Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
5            195             200             205

     cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc  672
     Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
             210             215             220
10

     ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag  720
     Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
     225             230             235             240

15   ctg tac aag tga                                                   732
     Leu Tyr Lys


     <210> 106
20   <211> 243
     <212> PRT
     <213> Artificial Sequence


     <400> 106
25   Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
      1               5                   10                  15

     Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                 20                  25                  30
30

     Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35                  40                  45

     Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
35      50                  55                  60

     Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
     65                  70                  75                  80

40   Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                     85                  90                  95

     Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                 100                 105                 110
45
     Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                 115                 120                 125

     Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
50       130                 135                 140

     Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
     145                 150                 155                 160

55   Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                     165                 170                 175

     Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                 180                 185                 190
60
     Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                 195                 200                 205

     Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
65       210                 215                 220

     Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
     225                 230                 235                 240

70   Leu Tyr Lys
```

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<210> 107
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Trp(TGG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 107
atg tgg tgg tgg tgg tgg agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Trp Trp Trp Trp Trp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1           5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc     624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc     672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag     720
```

```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240
```

5
```
ctg tac aag tga                                              732
Leu Tyr Lys
```

10
```
<210> 108
<211> 243
<212> PRT
<213> Artificial Sequence
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```
<400> 108
Met Trp Trp Trp Trp Trp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5               10              15
```
15

```
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30
```

20
```
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35              40              45
```

```
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60
```
25

```
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65              70              75              80
```

30
```
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85              90              95
```

```
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110
```

35
```
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115             120             125
```

```
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140
```
40

```
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160
```

```
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175
```
45

```
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190
```

50
```
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200             205
```

```
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220
```
55

```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240
```

```
Leu Tyr Lys
```
60

```
<210> 109
<211> 732
<212> DNA
<213> Artificial Sequence
```
65

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<220>
<223> Description of Artificial Sequence: Tyr(TAT)5GFP
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70
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<220>
<221> CDS
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<222> (1)..(732)

<400> 109

```
atg tat tat tat tat tat agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

<210> 110
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 110

```
Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1           5               10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
    65              70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235                 240

Leu Tyr Lys
```

<210> 111
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Val(GTA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 111

```
atg gta gta gta gta agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1           5               10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt  96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25                  30
```

```
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35              40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50              55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys


<210> 112
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 112
Met Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1             5               10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35              40                  45
```

```
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
            50                  55                  60

  5     Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
            65                  70                  75                  80

        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85                  90                  95

 10     Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                    100                 105                 110

        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                    115                 120                 125
 15
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                 135                 140

        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 20     145                 150                 155                 160

        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165                 170                 175

 25     Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180                 185                 190

        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195                 200                 205
 30
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210                 215                 220

        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 35     225                 230                 235                 240

        Leu Tyr Lys


 40     <210> 113
        <211> 732
        <212> DNA
        <213> Artificial Sequence

 45     <220>
        <223> Description of Artificial Sequence: Val(GTC)5GFP

        <220>
        <221> CDS
 50     <222> (1)..(732)

        <400> 113
        atg gtc gtc gtc gtc gtc agc aag ggc gag gaa ctg ttc act ggc gtg    48
        Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 55      1               5                  10                  15

        gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                    20                  25                  30
 60
        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                35                  40                  45

 65     ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
            50                  55                  60

        ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
 70     Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
            65                  70                  75                  80
```

```
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85                      90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                     105             110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                     120             125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                     135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                     150                     155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                     170                     175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                     185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                     200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210                     215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                     230                     235             240

ctg tac aag tga                                                     732
Leu Tyr Lys
```

<210> 114
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 114

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Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110
```

```
            Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                    115                 120                 125

  5         Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                    130                 135                 140

            Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
                    145                 150                 155                 160
 10
            Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                            165                 170                 175

            Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
 15                         180                 185                 190

            Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195                 200                 205

 20         Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                    210                 215                 220

            Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
            225                 230                 235                 240
 25
            Leu Tyr Lys
```

```
 30         <210> 115
            <211> 732
            <212> DNA
            <213> Artificial Sequence

            <220>
 35         <223> Description of Artificial Sequence: Val(GTG)5GFP

            <220>
            <221> CDS
            <222> (1)..(732)
 40
            <400> 115
            atg gtg gtg gtg gtg gtg agc aag ggc gag gaa ctg ttc act ggc gtg     48
            Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
             1               5                  10                  15
 45
            gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt     96
            Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                        20                  25                  30

 50         tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
            Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                        35                  40                  45

            ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
 55         Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                    50                  55                  60

            ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
            Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 60          65                  70                  75                  80

            gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
            Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                            85                  90                  95
 65
            tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
            Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                        100                 105                 110

 70         acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
            Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
```

```
                    115                    120                    125

        gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
    5   Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                    135                    140

        aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
            145                    150                    155                    160
   10

        aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                    165                    170                    175

   15   gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180                    185                    190

        atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
   20   Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195                    200                    205

        cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
   25       210                    215                    220

        ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225                    230                    235                    240
   30
        ctg tac aag tga                                                    732
        Leu Tyr Lys


   35   <210> 116
        <211> 243
        <212> PRT
        <213> Artificial Sequence

   40   <400> 116
        Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5                  10                     15

        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
   45                  20                  25                     30

        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35                  40                     45

   50   Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50                  55                  60

        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
        65                  70                  75                     80
   55
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85                  90                     95

        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
   60               100                    105                    110

        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                    115                    120                    125

   65   Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                    130                    135                    140

        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
   70       145                    150                    155                    160

        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
```

```
                         165                    170                    175
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180                    185                    190
 5
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195                    200                    205
10      Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                    210                    215                    220
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225                    230                    235                    240
15      Leu Tyr Lys


        <210> 117
        <211> 732
20      <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Description of Artificial Sequence: Val(GTT)5GFP
25
        <220>
        <221> CDS
        <222> (1)..(732)

30      <400> 117
        atg gtt gtt gtt gtt gtt agc aag ggc gag gaa ctg ttc act ggc gtg    48
        Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
         1               5                   10                  15

35      gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                    20                  25                  30

        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
40      Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                35                  40                  45

        ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
45         50                  55                  60

        ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
           65                  70                  75                  80
50
        gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                            85                  90                  95

55      tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                        100                 105                 110

        acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
60      Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                    115                 120                 125

        gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
65             130                 135                 140

        aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                 150                 155                 160
70
        aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
```

```
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165             170             175

  5     gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                        180             185             190

        atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
 10     Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                        195             200             205

        cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                        210             215             220
 15
        ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
        Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
        225                 230             235             240

 20     ctg tac aag tga                                                   732
        Leu Tyr Lys


        <210> 118
 25     <211> 243
        <212> PRT
        <213> Artificial Sequence

        <400> 118
 30     Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5               10              15

        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                        20              25              30
 35
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35              40              45

        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
 40           50              55              60

        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
        65              70              75              80

 45     Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85              90              95

        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                        100             105             110
 50
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                        115             120             125

        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
 55           130             135             140

        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145             150             155             160

 60     Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165             170             175

        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                        180             185             190
 65
        Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                        195             200             205

        Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 70                     210             215             220
```

```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

Leu Tyr Lys


<210> 119
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GFP humanized
      control

<220>
<221> CDS
<222> (1)..(717)

<400> 119
atg agc aag ggc gag gaa ctg ttc act ggc gtg gtc cca att ctc gtg    48
Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1               5                  10                  15

gaa ctg gat ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag    96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20                  25                  30

ggt gaa ggt gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc   144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

acc act gga aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc   192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50                  55                  60

tct tat ggc gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag   240
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65                  70                  75                  80

cat gac ttt ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga   288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

acc atc ttt ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc   336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
                100                 105                 110

aag ttc gaa ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att   384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
            115                 120                 125

gac ttt aag gag gat gga aac att ctc ggc cac aag ctg gaa tac aac   432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

tat aac tcc cac aat gtg tac atc atg gcc gac aag caa aag aat ggc   480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg   528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175

cag ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct   576
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180                 185                 190

gtg ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct   624
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
            195                 200                 205
```

```
aaa gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg    672
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210             215             220

acc gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga        717
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225             230             235
```

<210> 120
<211> 238
<212> PRT
<213> Artificial Sequence

<400> 120

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
  1             5               10                  15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20              25              30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35              40              45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50              55              60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65              70              75              80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
            85              90              95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100             105             110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
    115             120             125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130             135             140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145             150             155             160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
            165             170             175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180             185             190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
    195             200             205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210             215             220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225             230             235
```

<210> 121
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ala(GCA)5
      primer

<400> 121
cggggtacca tggcagcagc agcagca<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 122
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ala(GCC)5
      primer

<400> 122
cggggtacca tggccgccgc cgccgcc<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 123
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ala(GCG)5
      primer

<400> 123
cggggtacca tggcggcggc ggcggcg<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 124
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ala(GCT)5
      primer

<400> 124
cggggtacca tggctgctgc tgctgct<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 125
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(AGA)5
      primer

<400> 125
cggggtacca tgagaagaag aagaaga<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 126
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(AGG)5
      primer

<400> 126
cggggtacca tgaggaggag gaggagg<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 127
<211> 54

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(CGA)5
      primer

<400> 127
cggggtacca tgcgacgacg acgacgaagc aagggcgagg aactgttcac tggc          54


<210> 128
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(CGC)5
      primer

<400> 128
cggggtacca tgcgccgccg ccgccgcagc aagggcgagg aactgttcac tggc          54


<210> 129
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Arg(CGG)5
      primer

<400> 129
cggggtacca tgcggcggcg gcggcggagc aagggcgagg aactgttcac tggc          54


<210> 130
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<212> DNA
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<220>
<223> Description of Artificial Sequence: arg(CGT)5
      primer

<400> 130
cggggtacca tgcgtcgtcg tcgtcgtagc aagggcgagg aactgttcac tggc          54


<210> 131
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Asn(AAC)5
      primer

<400> 131
cggggtacca tgaacaacaa caacaacagc aagggcgagg aactgttcac tggc          54


<210> 132
<211> 54
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<220>
<223> Description of Artificial Sequence: Asn(AAT)5
      primer
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<210> 133
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<220>
<223> Description of Artificial Sequence: Asp(GAC)5
      primer

<400> 133
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<220>
<223> Description of Artificial Sequence: Asp(GAT)5
      primer

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<212> DNA
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<220>
<223> Description of Artificial Sequence: Cys(TGC)5
      primer

<400> 135
cggggtacca tgtgctgctg ctgctgcagc aagggcgagg aactgttcac tggc          54
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<210> 136
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<220>
<223> Description of Artificial Sequence: Cys(TGT)5
      primer

<400> 136
cggggtacca tgtgttgttg ttgttgtagc aagggcgagg aactgttcac tggc          54
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<210> 137
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Gln(CAA)5
      primer

<400> 137
cggggtacca tgcaacaaca acaacaaagc aagggcgagg aactgttcac tggc          54
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<210> 138
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<211> 54
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<220>
<223> Description of Artificial Sequence: Gln(CAG)5
      primer

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<210> 139
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<220>
<223> Description of Artificial Sequence: Glu(GAA)5
      primer

<400> 139
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<210> 140
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Glu(GAG)5
      primer

<400> 140
cggggtacca tggaggagga ggaggagagc aagggcgagg aactgttcac tggc   54

<210> 141
<211> 54
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<220>
<223> Description of Artificial Sequence: Gly(GGA)5
      primer

<400> 141
cggggtacca tgggaggagg aggaggaagc aagggcgagg aactgttcac tggc   54

<210> 142
<211> 54
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<220>
<223> Description of Artificial Sequence: Gly(GGC)5
      primer

<400> 142
cggggtacca tgggcggcgg cggcggcagc aagggcgagg aactgttcac tggc   54

<210> 143
<211> 54
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<220>
<223> Description of Artificial Sequence: Gly(GGG)5

primer

<400> 143
cggggtacca tggggggggg gggggggagc aagggcgagg aactgttcac tggc   54

<210> 144
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGT)5
      primer

<400> 144
cggggtacca tgggtggtgg tggtggtagc aagggcgagg aactgttcac tggc   54

<210> 145
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: His(CAC)5
      primer

<400> 145
cggggtacca tgcaccacca ccaccacagc aagggcgagg aactgttcac tggc   54

<210> 146
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: His(CAT)5
      primer

<400> 146
cggggtacca tgcatcatca tcatcatagc aagggcgagg aactgttcac tggc   54

<210> 147
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATA)5
      primer

<400> 147
cggggtacca tgataataat aataataagc aagggcgagg aactgttcac tggc   54

<210> 148
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATC)5
      primer

<400> 148
cggggtacca tgatcatcat catcatcagc aagggcgagg aactgttcac tggc   54

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<210> 149
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATT)5
      primer

<400> 149
cggggtacca tgattattat tattattagc aagggcgagg aactgttcac tggc          54


<210> 150
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTA)5
      primer

<400> 150
cggggtacca tgctactact actactaagc aagggcgagg aactgttcac tggc          54


<210> 151
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTC)5
      primer

<400> 151
cggggtacca tgctcctcct cctcctcagc aagggcgagg aactgttcac tggc          54


<210> 152
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTG)5
      primer

<400> 152
cggggtacca tgctgctgct gctgctgagc aagggcgagg aactgttcac tggc          54


<210> 153
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTT)5
      primer

<400> 153
cggggtacca tgcttcttct tcttcttagc aagggcgagg aactgttcac tggc          54


<210> 154
<211> 54
<212> DNA
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<220>
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<223> Description of Artificial Sequence: Leu(TTA)5
      primer

<400> 154
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<210> 155
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(TTG)5
      primer

<400> 155
cggggtacca tgttgttgtt gttgttgagc aagggcgagg aactgttcac tggc   54

<210> 156
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Lys(AAA)5
      primer

<400> 156
cggggtacca tgaaaaaaaa aaaaaaaagc aagggcgagg aactgttcac tggc   54

<210> 157
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Lys(AAG)5
      primer

<400> 157
cggggtacca tgaagaagaa gaagaagagc aagggcgagg aactgttcac tggc   54

<210> 158
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phe(CTT)5
      primer

<400> 158
cggggtacca tgcttcttct tcttcttagc aagggcgagg aactgttcac tggc   54

<210> 159
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Phe(TTC)5
      primer

<400> 159
cggggtacca tgttcttctt cttcttcagc aagggcgagg aactgttcac tggc   54

<210> 160
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CCC)5
      primer

<400> 160
cggggtacca tgccccccc cccccccagc aagggcgagg aactgttcac tggc   54

<210> 161
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CCG)5
      primer

<400> 161
cggggtacca tgccgccgcc gccgccgagc aagggcgagg aactgttcac tggc   54

<210> 162
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CCT)5
      primer

<400> 162
cggggtacca tgcctcctcc tcctcctagc aagggcgagg aactgttcac tggc   54

<210> 163
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CGA)5
      primer

<400> 163
cggggtacca tgcgacgacg acgacgaagc aagggcgagg aactgttcac tggc   54

<210> 164
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ser(AGC)5
      primer

<400> 164
cggggtacca tgagcagcag cagcagcagc aagggcgagg aactgttcac tggc   54

<210> 165
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ser(AGT)5
primer

5   <400> 165
cggggtacca tgagtagtag tagtagtagc aagggcgagg aactgttcac tggc   54

<210> 166
10   <211> 54
<212> DNA
<213> Artificial Sequence

<220>
15   <223> Description of Artificial Sequence: Ser(TCA)5
primer

<400> 166
cggggtacca tgtcatcatc atcatcaagc aagggcgagg aactgttcac tggc   54
20

<210> 167
<211> 54
<212> DNA
25 ·   <213> Artificial Sequence

<220>
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primer
30 ·
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cggggtacca tgtcctcctc ctcctccagc aagggcgagg aactgttcac tggc   54

35   <210> 168
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40   <220>
<223> Description of Artificial Sequence: Ser(TCG)5
primer

<400> 168
45   cggggtacca tgtcgtcgtc gtcgtcgagc aagggcgagg aactgttcac tggc   54

<210> 169
<211> 54
50   <212> DNA
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<220>
<223> Description of Artificial Sequence: Ser(TCT)5
55   primer

<400> 169
cggggtacca tgtcttcttc ttcttctagc aagggcgagg aactgttcac tggc   54

60
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65
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<223> Description of Artificial Sequence: Thr(ACA)5
primer

70   <400> 170
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<210> 171
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Thr(ACC)5
      primer

<400> 171
cggggtacca tgaccaccac caccaccagc aagggcgagg aactgttcac tggc   54

<210> 172
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thr(ACG)5
      primer

<400> 172
cggggtacca tgacgacgac gacgacgagc aagggcgagg aactgttcac tggc   54

<210> 173
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thr(ACT)5
      primer

<400> 173
cggggtacca tgactactac tactactagc aagggcgagg aactgttcac tggc   54

<210> 174
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Trp(TGG)5
      primer

<400> 174
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<210> 175
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Tyr(TAT)5
      primer

<400> 175
cggggtacca tgtattatta ttattatagc aagggcgagg aactgttcac tggc   54

<210> 176
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Val(GTA)5
       primer

<400> 176
cggggtacca tggtagtagt agtagtaagc aagggcgagg aactgttcac tggc   54

<210> 177
<211> 54
<212> DNA
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<220>
<223> Description of Artificial Sequence: Val(GTC)5
       primer

<400> 177
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<210> 178
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
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       primer

<400> 178
cggggtacca tggtggtggt ggtggtgagc aagggcgagg aactgttcac tggc   54

<210> 179
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Val(GTT)5
       primer

<400> 179
cggggtacca tggttgttgt tgttgttagc aagggcgagg aactgttcac tggc   54

<210> 180
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3'
       oligonucleotide common primer

<400> 180
ccggaattct cacttgtaca ggtggtccat gcc   33